Remarks

In the amendment herein, the specification has been amended to reflect additional sequence identifiers.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made." It is believed that no new matter has been introduced by the amendments.

Entry of these amendments is respectfully requested prior to examination.

Respectfully submitted,

GENENTECH, INC.

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By: _____

Paul Naik, Ph.D.
Reg. No. 49,075
Telephone: (650) 225-5530

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Paragraph beginning at line 16 of page 12 has been amended as follows:

Figure 13: Phage ELISAs for the display of a peptide fused to the C-terminus of protein VIII using poly-glycine linkers. A hexapeptide (HHHHHA **(SEQ ID NO. 279)**, referred to as a pentaHis flag) was fused to the C-terminus of protein VIII with intervening linkers containing varying numbers of Gly residues as indicated (linker length, X-axis). There is a large increase in display when the linker length is increased from eight to nine residues. The phage were used at a concentration of 2 x 10^{12} phage/mL. An anti-(His)5 antibody (Qiagen) was used as the capture target. See Example 22.

Paragraph beginning at line 32 of page 69 has been amended as follows:

LV: GAGGGCAGCTGTGGCTTCGGTGGCGGTVVCVVCVVCVVCVVCV **[~~(SEQ ID NO. 33)~~]**

Paragraph beginning at line 30 of page 78 has been amended as follows:

Standard molecular biology techniques were used to construct a phagemid designated pS1290a. pS1290a is identical to phagemid pS349 (see Example 8) except that the open reading frame (ORF) under the control of the IPTG-inducible Ptac promoter (New England Biolabs) has been deleted and replaced by a new ORF. The new ORF encodes a fusion product consisting of the maltose binding protein signal peptide, followed by a Ser residue, followed by residues 2-50 of mature protein VIII of *E. coli* bacteriophage M13. The ORF is followed by two TAA stop codons, followed by sequence (CACCATCACCATCACCATGCG) (SEQ ID NO: 108) encoding a heptapeptide (HHHHHHA **(SEQ ID NO. 280)**, hexaHis) flag or epitope tag, followed by two stop codons (TGATAA).

Paragraph beginning at line 1 of page 79 has been amended as follows:

pS1290a was mutated using the method of Kunkel (Example 12). The two TAA stop codons and the first His codon following the protein VIII C-terminus were replaced by various numbers of Gly codons. Appropriately designed and named mutagenic oligonucleotides were used (*e.g.*, oligonucleotide *G-6* inserts six Gly codons). This resulted in the construction of a series of phagemids encoding ORFs designed to secrete protein VIII molecules with C-terminal fusions consisting of linkers containing varying numbers of Gly residues followed by a pentaHis flag (HHHHHA **(SEQ ID NO. 279)**). The number of Gly residues was varied from zero (*i.e.*, the polyHis flag was fused directly to the protein VIII C-terminus) to 20. PentaHis flag display was measured by phage ELISA (Example 13) with an anti-(His)5 antibody (Qiagen) as the capture target (Fig. 13).

Paragraph beginning at line 41 of page 79 has been amended as follows:

Linkers selected for display of a peptide fused to the C-terminus of protein VIII. The sequences shown were inserted between the final residue of protein VIII and a heptapeptide (HHHHHHA **(SEQ ID NO. 280)**, referred to as a hexaHis flag). For each selectant, the DNA sequence is shown with the deduced amino acid sequence below. The numerical designation for each sequence is shown to the left.

Paragraph beginning at line 24 of page 80 has been amended as follows:

This ORF was designed as follows. The first two residues were (Met-Ser) chosen to allow good translation initiation. This dipeptide was followed by a retrotranslation of residues 40-48 of mature protein VIII from M13 bacteriophage (KLFKKFTSK **(SEQ ID NO. 282)** retrotranslated to KSTFKKFLK **SEQ ID NO. 283**) which was in turn

followed by a retrotranslation of protein VIII residues 1-20 (AEGDDPAKAAFNSLQASATE **(SEQ ID NO. 285)** retrotranslated to ETASAQLSNSAAKAPDDGEA **(SEQ ID NO. 284)**). To the C-terminus of this polypeptide was fused a nonapeptide (AAHHHHHHA **(SEQ ID NO. 281)**) hexaHis flag. Thus, this ORF consists of the dipeptide Met-Ser, followed by a retrotranslation of residues 1-48 of mature protein VIII with the central hydrophobic section (residues 21-30) deleted, followed by a hexaHis flag.

Paragraph beginning at line 26 of page 81 has been amended as follows:

Phagemid pS1232a was digested with *NsiI* and *XbaI* and a similarly digested DNA fragment encoding an hGH variant (hGH supermutant, hGHsm) with improved afffinity for the hGH binding protein (hGHbp) was inserted. The phagemid was designated pS1239b; it contains an ORF encoding P12-1 followed by a tetrapeptide linker (Ala-Ala-Asp-Ala), followed by hGHsm as shown below. The protein product of the pS1239b ORF is depicted; it consists of P12-1, followed by a tetrapeptide linker (AADA **(SEQ ID NO. 286)**), followed by hGHsm. P12-1 was divided into six zones as indicated, and a library was constructed for each zone. In addition, a linker library was constructed in which random 14-residue peptides were inserted in the middle of the tetrapeptide linker as shown.

Paragraph beginning at line 9 of page 83 has been amended as follows:

ATG	AGC	AAG	AGC	ACT	TTC	AAA	AAG	TTT	CTG
M	S	K	S	T	F	K	K	F	L

AAA	GTT	TTT	GTT	TTT	TCT	GTT	GAT	GTT	GAT
K	V	F	V	F	S	V	D	V	D

AAT	AAT	TGG	ATT	TGG	GCT	GTC	GGT	ATT	ATT	
N	N	W	I	W	A	V	G	I	I	
TAC	ATG	CTC	CTC	GTG	GAG	GCG	TCG	CCC	TGG	
Y	M	L	L	V	E	A	S	P	W	
GCT	GCT	AAG	GCG	CCA	GAC	GAT	GGT	GAA	GCT	**(SEQ ID NO. 124)**
A	A	K	A	P	D	D	G	E	A	**(SEQ ID NO. 33**)

~~(SEQ ID NO. 124)~~

Paragraph beginning at line 23 of page 84 has been amended as follows:

Standard molecular biology techniques were used to construct a phagemid designated pS1428d. Phagemid pS1428d is similar to pS1290a, except that the ORF under the control of the IPTG-inducible Ptac promoter (New England Biolabs) consists of the maltose binding protein signal peptide followed by the C-terminal domain of M13 protein III (Lowman *et al.*, (1991) *Biochemistry,* 30:10832). The method of Kunkel (Example 12) was used to fuse libraries to the C-terminus of the protein III C-terminal domain encoded by pS1428d. The libraries consisted of random linkers of various lengths followed by a hexaHis flag (HHHHHH **(SEQ ID NO. 287)**). The end result was libraries containing ORFs which encoded the C-terminal domain of protein III, followed by random polypeptide linker sequences, followed by the hexaHis flag. The lengths of the linkers were varied and depended on the mutagenic oligonucleotides used: oligonucleotides *UHg3-L6*, *UHg3-L8*, or *UHg3-L10* introduced linkers containing 6, 8, or 10 residues respectively. The diversities of the libraries were as follows: *UHg3-L6*, 3.5×10^{10}; *UHg3-L8*, 1.2×10^{10}; *UHg3-L10*, 2.8×10^{10}.